

SEQLIST.TXT

SEQUENCE LISTING

<110> Barsova, Ekaterina V.
LUKYANOV, SERGEY ANATOLIEVICH

<120> FLUORESCENT PROTEINS FROM COPEPODA
SPECIES AND METHODS FOR USING SAME

<130> EURE-005

<140> 10/533,781

<141> 2005-10-19

<150> 60/436,857

<151> 2002-12-26

<150> 60/459,679

<151> 2003-04-02

<150> RU03/00525

<151> 2003-11-26

<160> 30

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Pontellina plumata

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gtgggtatga	gaatcccttc	ctgcattgctg	ccaaacaagg	gggggtacac	aacaccagga	300
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tcaccgacaa	gatcatccgg	tccaatgcta	ccgtggagca	cttgaccaca	atggggagaca	480
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tgaaccacat	cagacgaata	acttgattct	aaaattatat	gaattttcaa	acaaaaaat	960
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<210> 2

<211> 222

<212> PRT

<213> Pontellina plumata

<400> 2

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		20						25					30		

SEQLIST.TXT

Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
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 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
 50 55 60
 Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn
 65 70 75 80
 Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
 85 90 95
 Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
 100 105 110
 Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
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 Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Thr Phe Ser Leu
 145 150 155 160
 Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe
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 Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

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 <213> Pontellina plumata

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 ctcttgagca gggagctatg accaacaaga tgaagtctac caaggggcgcc ttgaccttct 180
 cccctacctt tctctctcat gtcatgggat acgggttcta ccactttggt acctatccca 240
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 <212> PRT
 <213> Pontellina plumata

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 35 40 45
 Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly

SEQLIST.TXT

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				85							90					95	
	Leu	His	Val	Ser	Phe	Ser	Tyr	Arg	Tyr	105	Glu	Ala	Gly	Arg	Val	Ile	Gly
	Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	120	Pro	Glu	Asp	Ser	Val	Ile	Phe
	Thr	Asp	Lys	Ile	Ile	Arg	Ser	Asn	Ala	135	Thr	Val	Glu	His	Leu	His	Pro
	Met	Gly	Asp	Asn	Val	Leu	Val	Gly	Ser	150	Phe	Ala	Arg	Thr	Phe	Ser	Leu
145	Arg	Asp	Gly	Gly	Tyr	Ser	Phe	Val	Val	165	Asp	Ser	His	Met	His	175	Phe
	Lys	Ser	Ala	Ile	His	Pro	Ser	Ile	Leu	180	Gln	Asn	Gly	Gly	Pro	Met	Phe
	Ala	Phe	Arg	Arg	Val	Glu	Glu	Leu	His	185	Ser	Asn	Thr	Glu	Leu	Gly	Ile
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<210> 5
 <211> 814
 <212> DNA
 <213> Labidocera aestiva

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	gatggaaca	catgatgaag	acgtatgacc	aacaagatga	agtccacca	aggacctctc	180
	tccttctctc	cttacctact	ctccacatc	atgggctacg	gattctatca	ctatgctacc	240
	ttccctgtcg	gatatgagaa	tgcttacctc	catgctgcta	agaattggagg	ctacaccaac	300
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	gttatcttca	ctgacaagat	catcaagtcc	aaccacaact	gtgagcacat	ctaccccaag	480
	ggagataata	ttcttgtcaa	tgcttacctc	cgaacttggg	tgctgagaga	tggtggatcc	540
	tactctgcac	agggtcaaca	tcatctccac	ttcaagactg	ccatgcatcc	caccatgctc	600
	cagaacggag	gatccatggt	tacctacagg	aagggttgagg	agctccacag	ccagtcagat	660
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	aaatatgtgt	ccatctcagac	aattaataca	ataaaccttta	cttatcattg	taaaaacaaa	780
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<210> 6
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 <212> PRT
 <213> Labidocera aestiva

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				20					25							
	Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser
				35				40						45		
	Pro	Tyr	Leu	Leu	Ser	His	Ile	Met	Gly	Tyr	Gly	Phe	Tyr	His	Tyr	Ala
	Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Val	Tyr	Leu	His	Ala	Ala	Lys	Asn
65	Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
				85					90					95		
	Ile	Ser	Val	Asn	Phe	Thr	Tyr	Arg	Tyr	Glu	Gly	Asn	Lys	Val	Ile	Gly

SEQLIST.TXT

Asp	Phe	Lys	100	Val	Val	Gly	Ser	Gly	105	Phe	Pro	Ala	Asn	110	Ser	Val	Ile	Phe
Thr	Asp	Lys	115	Ile	Ile	Lys	Ser	Asn	120	Pro	Thr	Cys	Glu	125	His	Ile	Tyr	Pro
Lys	Gly	Asp	130	Asn	Ile	Leu	Val	Asn	135	Ala	Tyr	Thr	Arg	140	Thr	Trp	Met	Leu
Arg	Asp	Gly	145	Gly	Tyr	Tyr	Ser	Ala	150	Gln	Val	Asn	Asn	155	His	Leu	His	Phe
Lys	Thr	Ala	165	Met	His	Pro	Thr	Met	170	Gln	Asn	Gly	Gly	175	Ser	Met	Phe	
Thr	Tyr	Arg	180	Lys	Val	Glu	Glu	Leu	185	His	Ser	Gln	Ser	190	Asp	Val	Gly	Ile
Val	Glu	Tyr	195	Gln	His	Val	Phe	Lys	200	Thr	Pro	Thr	Ala	205	Phe	Ala		
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<210> 7

<211> 753

<212> DNA

<213> cf. *Pontella meadi* Wheeler

<400> 7

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atacagatga	gggacgcgatg	accaacaaaa	tgaagtccat	caaaggacct	atctccttct	180
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ctggatatga	aaatatctac	cttcatgccca	tgaagaatgg	aggttactcc	aatgtcagaa	300
ctgagaggta	tgaggatgga	ggcatcattt	ctataacctt	caactacaga	tatgaaggga	360
acaagatcat	tgagagcttc	aaggtgtgtg	gaacaggatt	ccctaccaca	agttcttatct	420
tcactgacaa	gaatcattaaa	tccaacccta	ctgtgagaaa	catgttcccc	aaggctgaca	480
atactcttgt	gaatgcctac	accagaacat	atttgtctaa	agatgggtgga	tactactctg	540
cccagggttaa	caaccatgat	cacttcaaga	gtgccatcca	taccacatgt	ctccagaatg	600
gcggatccat	gttcacctac	agagttgtag	aggagacaca	cactcagaac	gaagtgtcta	660
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<210> 8

<211> 222

<212> PRT

<213> cf. *Pontella meadi* Wheeler

<400> 8

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Glu	Glu	Phe	Glu	Leu	Ile	Gly	Ala	Gly	Asp	Gly	Asn	Thr	Asp	Glu	Gly
			20					25					30		
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Ile	Lys	Gly	Pro	Ile	Ser	Phe	Ser
			35				40						45		
Pro	Tyr	Leu	Leu	Ser	His	Ile	Leu	Gly	Tyr	Gly	Tyr	Tyr	His	Phe	Ala
			50				55				60				
Thr	Phe	Pro	Ala	Gly	Tyr	Glu	Asn	Ile	Tyr	Leu	His	Ala	Met	Lys	Asn
					70					75				80	
Gly	Gly	Tyr	Ser	Asn	Val	Arg	Thr	Glu	Arg	Tyr	Glu	Asp	Gly	Gly	Ile
				85					90					95	
Ile	Ser	Ile	Thr	Phe	Asn	Tyr	Arg	Tyr	Glu	Gly	Asn	Lys	Ile	Ile	Gly
				100				105					110		
Asp	Phe	Lys	Val	Val	Gly	Thr	Gly	Phe	Pro	Thr	Asn	Ser	Leu	Ile	Phe
			115				120					125			
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Thr	Cys	Glu	Asn	Met	Phe	Pro
			130				135				140				
Lys	Ala	Asp	Asn	Thr	Leu	Val	Asn	Ala	Tyr	Thr	Arg	Thr	Tyr	Leu	Leu
			145		150					155				160	

SEQLIST.TXT

Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile
 195 200 205
 Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
 210 215 220

<210> 9
 <211> 880
 <212> DNA
 <213> cf. Pontella meadi Wheeler

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 tcaaaaatgcc tgacatgaag cttgagtgcc acatctccgg aacctgaat ggagaggagt 180
 ttgaacttat tggttctgga gatggaaata ctgacgagg acgcatgaca aacaatatga 240
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 agaatggagg ttactcaaat gtcaggactg agaggtatga ggaatggaggc atcattttcta 420
 taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa 480
 caggattccc taccgacagt cttatcttca ctgacaagat cattaaatcc aaccttacct 540
 gcgagaacat gttccccaag gctgacaaca ttcttggtaa tgcctacacc agaacctatt 600
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 ccatccatcc tacaatgctc cagaatgggt gatccattgt cactcacaga gtatagagg 720
 agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta 780
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 gcatttttat aatgcataga aaaaataatg tatattttat 880

<210> 10
 <211> 222
 <212> PRT
 <213> cf. Pontella meadi Wheeler

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 20 25 30
 Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser
 35 40 45
 Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
 50 55 60
 Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
 65 70 75 80
 Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
 85 90 95
 Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly
 100 105 110
 Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe
 115 120 125
 Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
 130 135 140
 Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
 145 150 155 160
 Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
 165 170 175
 Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
 180 185 190
 Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile

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195 200 205
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
210 215 220

<210> 11
<211> 847
<212> DNA
<213> Pontella mediterranea

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tttgaaacttg ttgggtgctgg agaagggaaac actgatgagg gacgcatgac caacaagatg 180
aagtcaccca aggggacctct ttctctctct ccttatitgc tctccacgt tcttggttat 240
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aagaatggag gttactccaa cacaagaact gagaggtagt aggatggagg tatcatttct 360
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acgggattcc ctgccgacag catcatcttc actgacaaga tcatcaagtc caacctacc 480
tgtgagcaca tctaccceaa ggctaacaat attcttgtga atgcttacac cagaacctgg 540
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<211> 222
<212> PRT
<213> Pontella mediterranea

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20 25 30
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35 40 45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
50 55 60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65 70 75 80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
85 90 95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
100 105 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
115 120 125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
130 135 140
Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145 150 155 160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu
165 170 175
Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe
180 185 190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
195 200 205
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
210 215 220

SEQLIST.TXT

<210> 13
 <211> 850
 <212> DNA
 <213> Pontella mediterranea

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<400> 13
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tttgaacttg ttggtgctgg agatggaaac actgatgagg gacgcgatgac caaccagatg 180
aagtccacaa agggacctct ctctcttctc cctcacttgc tctccacgt tcttggctat 240
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acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgcctttatg 780
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<210> 14
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 <212> PRT
 <213> Pontella mediterranea

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20      25      30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
50      55      60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65      70      75
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
85      90      95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
100     105     110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
115     120     125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
130     135     140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145     150     155
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
165     170     175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
180     185     190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
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Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
210     215     220
  
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 <213> Unknown

SEQLIST.TXT

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<223> unidentified Pontellidae species

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ggaaatactg	atcaggggacg	tatgaccaac	aagatgaaat	ctaccaaggg	tccactctcc	180
ttctctccct	atcttctctc	tcatgtcatg	ggatattggt	tctatcattt	tgggaacattt	240
ccagtggtt	atgagaatcc	ctatgtccac	gccatgacga	acgggtggata	taccaacacc	300
aggattgaaa	gttatgaaga	tggaggtgtt	ctttacctta	ccttcaacta	cagatttggt	360
ggaaacaaga	ttatcgggga	cttcaagtgt	gtcggaaactg	gattccctga	ggacagcgtt	420
atcttctactg	acaagatcat	caagtcaca	cccaattgtg	aacattttcta	tcacaatggt	480
gaaacaatca	tgaataatgc	ctacatgaga	actctctccc	tcagagatgg	tggctactac	540
tctggtccagg	ttaccagcca	catccacttc	aagaatgcga	tccacccatc	catcctctat	600
aacggcggtat	ccatgtttcac	ctacagaaga	gttgaggagc	tccacactca	aactgatctt	660
ggaattgttg	agtaccagca	tgtattcaag	actcccactg	cttttgcttg	aatgccatga	720
agatgaaacc	tgaacaagat	caatctttat	ttaccacaat	atgtaaatgg	tttaattgta	780
taattctcga	gaattcatat	aatacataga	atttatctta	c		821

<210> 16

<211> 222

<212> PRT

<213> Unknown

<220>

<223> unidentified Pontellidae species

<400> 16

Met	Ala	Ala	Met	Lys	Ile	Glu	Cys	Arg	Ile	Thr	Gly	Thr	Met	Asn	Gly	
1				5					10					15		
Val	Glu	Phe	Glu	Leu	Val	Gly	Gly	Gly	Glu	Gly	Asn	Thr	Asp	Gln	Gly	
			20					25					30			
Arg	Met	Thr	Asn	Lys	Met	Lys	Ser	Thr	Lys	Gly	Pro	Leu	Ser	Phe	Ser	
			35					40				45				
Pro	Tyr	Leu	Leu	Ser	His	Val	Met	Gly	Tyr	Gly	Phe	Tyr	His	Phe	Gly	
			50				55				60					
Thr	Phe	Pro	Ser	Gly	Tyr	Glu	Asn	Pro	Tyr	Val	His	Ala	Met	Thr	Asn	
			65			70				75					80	
Gly	Gly	Tyr	Thr	Asn	Thr	Arg	Ile	Glu	Ser	Tyr	Glu	Asp	Gly	Gly	Val	
				85				90					95			
Leu	Tyr	Leu	Thr	Phe	Asn	Tyr	Arg	Leu	Asp	Gly	Asn	Lys	Ile	Ile	Gly	
				100				105								
Asp	Phe	Lys	Cys	Val	Gly	Thr	Gly	Phe	Pro	Glu	Asp	Ser	Val	Ile	Phe	
				115			120					125				
Thr	Asp	Lys	Ile	Ile	Lys	Ser	Asn	Pro	Asn	Cys	Glu	His	Phe	Tyr	Pro	
				130			135				140					
Met	Ala	Glu	Asn	Ile	Met	Lys	Asn	Ala	Tyr	Met	Arg	Thr	Leu	Ser	Leu	
					150					155					160	
Arg	Asp	Gly	Gly	Tyr	Tyr	Ser	Gly	Gln	Val	Thr	Ser	His	Ile	His	Phe	
				165				170						175		
Lys	Asn	Ala	Ile	His	Pro	Ser	Ile	Leu	His	Asn	Gly	Gly	Ser	Met	Phe	
				180				185					190			
Thr	Tyr	Arg	Arg	Val	Glu	Glu	Leu	His	Thr	Gln	Thr	Asp	Leu	Gly	Ile	
				195			200					205				
Val	Glu	Tyr	Gln	His	Val	Phe	Lys	Thr	Pro	Thr	Ala	Phe	Ala			
				210			215				220					

<210> 17

<211> 669

<212> DNA

<213> Artificial Sequence

SEQLIST.TXT

<220>

<223> nucleic acid sequence for humanized version of
ppluGFP2

<400> 17

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atgcccgcca tgaagatcga gtgccgcac accggcacc tgaacggcgt ggagttcgag 60
ctggtggggc gcggagaggg caccctccg cagggccgca tgaccaacaa gatgaagagc 120
accaaggggc ccttgacctt cagcccttac ctgctgagcc acgtgatggg ctacggcttc 180
taccacttgc gcacctaccc cagcggctac gagaacccct tcctgcacgc catcaacaac 240
ggcggcttaca ccaacaccgc catcgagaag tacgaggacg gcggcgctgt gcacgtgagc 300
ttcagctacc gctacgaggg atcggcgact tcaaggtggg gggcaccggc 360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag 420
cacctgcacc ccatgggcga taacgtgctg gtgggcagct tcgcccgcac cttcagcctg 480
cgcgacggcg gctactacag cttcgtgtgt gacagccaca tgcacttcaa gagcgccatc 540
caccacagca tcctgcagaa cgggggcccc atgttcgcct tccgcgcggt ggaggagctg 600
cacagcaaca ccgagctggg catcgtggag taccagcac ctttcaagac cccgatcgca 660
ttcgctga

```

<210> 18

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for humanized version of
ppluGFP2

<400> 18

```

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20     25     30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35     40     45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50     55     60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65     70     75
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85     90     95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100    105    110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115    120    125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
130    135    140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145    150    155
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165    170    175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180    185    190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195    200    205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
210    215    220

```

<210> 19

<211> 589

<212> DNA

<213> Artificial Sequence

SEQLIST.TXT

<220>

<223> nucleic acid sequence for ppluGFP2 with
yeast-optimized codon usage

<400> 19

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tactccagaa caaggtagaa tgactaataa aatgaaatct actaaagggtg ctttgacttt 60
ttctccatat ttgttgcttc atgttaatggg ttaatggtttt tatcatctttg gtacttatcc 120
attctggttat gaaaatccat ttttgcatgc tattataaat ggttggttata ctaatactag 180
aattgaaaaa tatgaagatg gtggtgtttt gcatgtttct ttttcttata gatatgaagc 240
tggttagagtt attggcgatt ttaaagtgtt tggtagctggt ttccagaag attctgttat 300
ttttactgat aaaattatta gatctaattgc tactgttgaa catttgcac caatgggtga 360
taatgttttg gttggttctt ttgctagaac tttttctttg agagatgggtg gttattatttc 420
ttttgttgtt gatctcataa tgcattttaa atctgctatt catccatcta ttttgcacaaa 480
tgggtgtcca atgtttgctt ttagaagagt tgaagaattg catttcaata ctgaattggg 540
tattgttgaa tatcaacatg cttttaaac tcgaattgct ttgtcttaa 589
```

<210> 20

<211> 222

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for ppluGFP2 with
yeast-optimized codon usage

<400> 20

```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20      25      30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50      55      60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65      70      75      80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85      90      95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100     105     110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115     120     125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
130     135     140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145     150     155     160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165     170     175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180     185     190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195     200     205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
210     215     220
```

<210> 21

<211> 669

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence for CopCFP mutant
Page 10

SEQLIST.TXT

```

<400> 21
atgcccgcca tgaagatcga gtgccgcctc accggccacc tgaacggcgt ggagttcgag 60
ctggtggggc gcggaagagg caccctccag cagggccgca tgaccaacaa gatgaagagc 120
accaaaggcg ccttgacctt cagcccttac ctgctgagcc acgtgatggg ctggggcttt 180
taccactttc gcacctacc cagcggctac gagaacctct tcttgacgc calcaacaac 240
ggcggctaca ccaacaccg catcgagaag tacgaggacg gcggcgtgct gcacgtgagc 300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaagggtgt gggcaccggc 360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag 420
caccctgcgc ccatgggcga taactgtctg gtgggcagct tcgcccgcac cttcagcctg 480
cgcgacggcg gctactacag cttcgtgggt gacagccaca tgcacttcaa gagcgccatc 540
caccccagca tctctcagaa cgggggcccc atgttcgcct tccgcgcgtg ggaggagctg 600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca 660
ttcgccata

```

```

<210> 22
<211> 222
<212> PRT
<213> Artificial Sequence

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```

<220>
<223> polypeptide sequence for CopCFP mutant

```

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<400> 22
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1 5 10 15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
20 25 30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35 40 45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
50 55 60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65 70 75 80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85 90 95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100 105 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115 120 125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
130 135 140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145 150 155 160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165 170 175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180 185 190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195 200 205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
210 215 220

```

```

<210> 23
<211> 690
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> nucleic acid sequence for CopGFP-NAl mutant

```

```

<400> 23

```

SEQLIST.TXT

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ctgaaccggc tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggcgccg 120
atgaccaaca agatgaagag caccgaaggc gccctgacct tcagcccccta cctgctgagc 180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggccta cgagaacccc 240
ttcctgcacg ccatcaacaa cggcggctac accaacaccc gcacgcgaga gtacgaggac 300
ggcggcgctg tgacagttag ctctcagctac cgtcacgagg ccggccgcgt gatcgggcag 360
ttcaaggtag tgggcaccgg ctcccccgag gacagcgtga tcttcaccga caagatcatc 420
cgcagcaacg ccacgttgga gcacctgcac cccatggggc ataactgtgt ggtggggcagc 480
ttcgcccga ctttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat cccccccagc atcctgcaga acggggggccc catgttcgcc 600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcacgtgga gtaccagcac 660
gccttcaaga ccccgatcgc attccgctga

```

<210> 24

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for CopGFP-NA1 mutant

<400> 24

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Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1      5      10      15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly
20     25     30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
35     40     45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
50     55     60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Gly Tyr Glu Asn Pro
65     70     75     80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
85     90     95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
100    105    110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115    120
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130    135    140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145    150    155    160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
165    170    175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
180    185    190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
195    200    205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
210    215    220
Pro Ile Ala Phe Ala
225

```

<210> 25

<211> 819

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleic acid sequence for CopGFP-NA2 mutant

<400> 25

SEQLIST.TXT

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ctggtgggag cgaggagagg caccgccgag cagggccgca tgaccaacaa gatgaagagc 120
accaagggcg ccttgacctt cagcccccac ctgctgagcc acgtgatggg ctacgggttc 180
taccactttg gcacctacc cagcggctac gagaacccct tctctgacgc ctatcaacaac 240
ggcggctaca ccaacaccgc catcgagaag tacgaggacg cgggcgtgct gcacgtgagc 300
ttcagctacc gctacgaggc cgcccgctgt atcgcgact tcaaggtggt gggcaccggc 360
ttcccgagg acacgctgat ctccaccgac aagatcatcc gcagcaacgc caccgtggag 420
cacttcgacc ccatggcgga taactgtctg gtggcgactc tcgcccgcac ctctagcctg 480
cgcgacggcg gctactacag cttcgtgggt gacagccaca tgcaattcaa gagcgccatc 540
caccgccaga tctctcagaa cgggggcccc atgttcgcct tcgcccgcgt ggaggagctg 600
cacagcaaca cggagctggg catcgtggag taccagcac ccttcaagac ccgatcgca 660
ttcgccagat ccagagccca ggcagcaaac tccgcctggg atggcacagc cggaccggga 720
tcggccgcga ctctagatca taatcagcca taccacattt gtagagggtt tacttgcctt 780
aaaaaacctc ccacacctcc cctgaacctt gaaacataa 840

```

<210> 26

<211> 272

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for CopGFP-NA2 mutant

<400> 26

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Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1      5      10      15
Val Glu Phe Glu Leu Val Gly Gly Gly Thr Pro Glu Gln Gly
20      25      30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
35      40      45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
50      55      60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65      70      75      80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
85      90      95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
100     105     110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
115     120     125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
130     135     140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145     150     155     160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
165     170     175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
180     185     190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
195     200     205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser
210     215     220
Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly
225     230     235     240
Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly
245     250     255
Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
260     265     270

```

<210> 27

<211> 840

<212> DNA

SEQLIST.TXT

<213> Artificial Sequence

<220>

<223> nucleic acid sequence for CopGFP-NA3 mutant

<400> 27

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ctgaaccggc tggagttcga gctggtgggc gccggagagg gcaccccgca gcaggggcgc 120
atgaccaaca agatgaagag caccgaaggc gccctgacct cagcccgcta cctgctgagc 180
cacgtgatgg gctacggctt ctaccacttc gccacctacc ccagcggcta cgagaaaccc 240
ttccttcagg ccatcaacaa cggcggttac accaacaccc gcatcgagaa gtacgaggac 300
ggcggcggtc tgcacgtgag cttcagctac cgtcacgagg ccggccgcgt gatcggcgac 360
ttcaagggtg tgggcaccgg cttcccgagc gacagcgtga tcttcaccga caagatcatc 420
cgcagcaacg ccaccgtgga gcacctgcac ccatggggcg ataacgtgct ggtggggcgc 480
ttcgcgcgca ctttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac 540
atgcacttca agagcgccat ccaccccgag atcctgcaga acggggggccc catgttcgcc 600
ttccgcgcgc tggaggagct gcacagcaac accgagctgg gcatcggtga gtaccagcac 660
gccttcaaga ccccgatcgc attcgccaga tcagagccc aggcagcaa ctccgccgtg 720
gatggcacag ccggaccggg atcggccgcg actctagatc ataactagcc ataccacatt 780
tgtagaggtt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaaacataa 840

```

<210> 28

<211> 279

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide sequence for CopGFP-NA3 mutant

<400> 28

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Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1      5      10      15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
20      25
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
35      40      45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
50      55      60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65      70      75      80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
85      90      95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
100      105      110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
115      120      125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
130      135      140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145      150      155      160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
165      170      175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
180      185      190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
195      200      205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
210      215      220
Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
225      230      235      240
Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
245      250      255

```

SEQLIST.TXT

Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr
 260 265 270
 Pro Pro Pro Glu Pro Glu Thr
 275

<210> 29
 <211> 238
 <212> PRT
 <213> Aequorea Victoria

<400> 29
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 30
 <211> 225
 <212> PRT
 <213> Discosoma sp.

<400> 30
 Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val
 1 5 10 15
 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
 20 25 30
 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
 35 40 45
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
 50 55 60
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser

SEQLIST.TXT

100										105										110									
Leu	Gln	Asp	Gly	Cys	Phe	Ile	Tyr	Met	Lys	Val	Lys	Phe	Ile	Gly	Val	Asn													
Phe	Pro	Ser	Asp	Gly	Pro	Val	Met	Gln	Lys	Lys	Lys	Thr	Met	Gly	Trp	Glu													
Ala	Ser	Thr	Glu	Arg	Leu	Tyr	Pro	Arg	Asp	Gly	Gly	Val	Leu	Lys	Gly	Glu													
Ile	His	Lys	Ala	Leu	Lys	Leu	Lys	Asp	Gly	Gly	His	Tyr	Leu	Val	Glu														
Phe	Lys	Ser	Ile	Tyr	Met	Ala	Lys	Lys	Pro	Val	Gln	Leu	Pro	Gly	Tyr														
Tyr	Tyr	Val	Asp	Ser	Lys	Leu	Asp	Ile	Thr	Ser	His	Asn	Glu	Asp	Tyr														
Thr	Ile	Val	Glu	Gln	Tyr	Glu	Arg	Thr	Glu	Gly	Arg	His	His	Leu	Phe														
Leu																													